

***Xylodon flocculosus* sp. nov. from Yunnan, China**

MENG-HAN QU^{1,3} & CHANG-LIN ZHAO^{1,2,4*}

¹ Key Laboratory for Forest Resources Conservation and Utilization in the
Southwest Mountains of China, Ministry of Education, Southwest Forestry University,
Kunming 650224, P.R. China

² College of Biodiversity Conservation, Southwest Forestry University,
Kunming 650224, P.R. China

³ College of Forestry, Southwest Forestry University, Kunming 650224, P.R. China

⁴ Yunnan Key Laboratory for Fungal Diversity and Green Development,
Kunming Institute of Botany, Chinese Academy of Science,
Kunming 650201, China

* CORRESPONDENCE TO: fungichanglinz@163.com

ABSTRACT —A new corticioid fungal species, *Xylodon flocculosus*, is described from China based on morphological and ITS+LSU sequence analyses.

KEY WORDS — Honghe county, *Hymenochaetales*, *Schizoporaceae*, taxonomy, wood-rotting fungi

Introduction

The corticioid genus *Xylodon* (Pers.) Gray, with *X. quercinus* (Pers.) Gray as the type, is widespread. Its species are primarily wood decomposers causing white rot of both angiosperms and gymnosperms (Eriksson & Ryvar den 1976, Yurchenko & Wu 2014), although a few *Xylodon* taxa have also been collected on brown rotten spruce stumps, palms or palm tree inflorescences, bamboo, and ferns (Burdsall & al. 1981, Langer 1994, Nordén & al. 1999, Kotiranta & Saarenoksa 2000, Boidin & Gilles 2003, Hjortstam & al. 2005, Xiong & al. 2010, Jo & al. 2019). The genus is characterized by resupinate basidiomata with hymenophores that are smooth, tuberculate,

grandinioid, odontoid, coralloid, irpicoid or poroid; a monomitic hyphal system with clamp connections on generative hyphae; cystidia that are bladder-like, bottle-shaped, and capitate to subulate; suburniform basidia; and globose to ellipsoid to cylindrical basidiospores (Gray 1821, Bernicchia & Gorjón 2010). Index Fungorum (<http://www.indexfungorum.org>) lists 192 specific and infraspecific names in *Xylodon*, but currently accepted number of species in the genus is about 90 (Wu 1990, 2000, 2001, 2006; Xiong & al. 2009, 2010; Dai 2011, 2012; Lee & Langer 2012; Yurchenko & al. 2013; Yurchenko & Wu 2014; Zhao & al. 2014; Chen & al. 2016, 2018; Kan & al. 2017a,b; Riebesehl & Langer 2017; Wang & Chen 2017; Shi & al. 2019; Ma & Zhao 2021). About 22 *Xylodon* species have been found and described in China (Wang & Chen 2017, Shi & al. 2019, Ma & Zhao 2021, Wang & al. 2021).

Yurchenko & Wu (2014) placed *Xylodon* in the *Xylodon-Schizopora-Palifer* clade based on nuclear DNA sequence studies of *Hyphodontia* s.l. In their studies based on morphological and molecular analyses Riebesehl & Langer (2017) proposed 16 new *Xylodon* combinations. Riebesehl & al. (2019), who accept 77 species in the genus, synonymised *Palifer* Stalpers & P.K. Buchanan and *Odontiopsis* Hjortstam & Ryvarden with *Xylodon*.

We encountered an undescribed taxon during our research on corticioid fungi in southern China. Morphological comparisons and internal transcribed spacer (ITS) and large subunit nuclear ribosomal RNA gene (nLSU) sequence analyses place the fungus in *Xylodon*. The taxon is proposed here as *Xylodon flocculosus*.

Materials & methods

The studied specimens have been deposited at the herbarium of Southwest Forestry University, Kunming, Yunnan Province, P.R. China (SWFC). Macromorphological descriptions are based on field notes. Colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under a light microscope following Dai (2012). The following abbreviations are used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both non-amyloid and non-dextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n = number of spores measured/number of specimens.

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd.) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions. The ITS region was amplified with primer pairs ITS5

TABLE 1. *Hastodontia*, *Lyomyces*, and *Xylodon* species and sequences used in the phylogenetic analyses.

SPECIES	SAMPLE	GENBANK ACCESSION NO.		REFERENCE
		ITS	LSU	
<i>H. halonata</i>	Mexico	MK575207	MK598738	Yurchenko & al. 2020
<i>H. hastata</i>	KHL14646	MH638232	MH638232	Viner & al. 2018
<i>L. allantosporus</i>	FR-0249548	KY800397	KY795963	Yurchenko & al. 2017
<i>L. mascarensis</i>	KAS-GEL 4833	KY800399	KY795964	Yurchenko & al. 2017
<i>L. organensis</i>	MSK 7247	KY800403	KY795967	Yurchenko & al. 2017
<i>L. orientalis</i>	GEL 3400	DQ340326	DQ340353	Yurchenko & al. 2017
<i>X. apacheriensis</i>	Wu 0910-58	KX857797	KX857822	Chen & al. 2017
<i>X. asper</i>	GEL 3257	EU583424	—	Yurchenko & al. 2020
<i>X. astrocystidiatus</i>	Wu 9211-71	JN129972	JN129973	Yurchenko & Wu 2014
<i>X. australis</i>	CANB869100	MT158715	MT158751	Fernández-López & al. 2020
<i>X. borealis</i>	Spirin 9416	MH317760	MH638259	Viner & al. 2018
<i>X. brevisetus</i>	KHL 12386	DQ873612	DQ873612	Larsson & al. 2006
<i>X. bubalinus</i>	Cui 12888	NR_154097	—	Wang & Chen 2017
<i>X. chinensis</i>	Wu 1407-105	KX857804	KX857811	Chen & al. 2017
<i>X. cystidiatus</i>	FR-0249200	MH880195	MH884896	Riebesehl & al. 2019
<i>X. detriticus</i>	Zíbarová 16.05.17	MH320794	—	Viner & al. 2018
<i>X. exilis</i>	MSK-F 7381	MH880196	MH884897	Riebesehl & al. 2019
<i>X. filicinus</i>	FR-0249797	MH880201	MH884901	Riebesehl & al. 2019
<i>X. flocculosus</i>	CLZhao 4544	MW980775	—	Present study
	CLZhao 18342 [T]	MW980776	MW980779	Present study
	CLZhao 18379	MW980777	MW980780	Present study
	CLZhao 18394	MW980778	MW980781	Present study
<i>X. follis</i>	FR-0249814	MH880204	MH884902	Riebesehl & al. 2019
<i>X. hastifer</i>	Ryvarden 19767	KY081801	—	Riebesehl & Langer 2017
<i>X. heterocystidiatus</i>	Wu 9209-27	JX175045	KX857821	Chen & al. 2017
<i>X. hyphodontinus</i>	LIP GG-MAR15-127	MH880208	MH884906	Riebesehl & al. 2019
<i>X. kunmingensis</i>	CLZhao 755	MK404530	—	Shi & al. 2019
<i>X. lenis</i>	Wu890714-3	KY081802	—	Riebesehl & Langer 2017
<i>X. mollis</i>	Wu 0808-32	JX175043	KX857820	Chen & al. 2017

SPECIES	SAMPLE	GENBANK ACCESSION NO.		REFERENCE
		ITS	LSU	
<i>X. mollissimus</i>	Yuan 4391	KY007518	—	Kan & al. 2017b
<i>X. nesporii</i>	MA:Fungi:79920	MT158717	MT158753	Fernández-López & al. 2020
<i>X. niemelaei</i>	Wu 1010-62	KX857799	KX857817	Chen & al. 2017
<i>X. nongravis</i>	GC 1412-22	KX857801	KX857818	Chen & al. 2017
<i>X. nothofagi</i>	PDD: 91630	GQ411524	—	Fukami & al. 2010
<i>X. ovisporus</i>	SFC20180822-22	MK992859	—	Lupala & al. 2019
<i>X. paradoxus</i>	KAS-JR06	MH880219	—	Riebesehl & al. 2019
<i>X. pseudotropicus</i>	Dai 10768	NR_154066	—	Zhao & al. 2014
<i>X. quercinus</i>	MA:Fungi:84446	MT158719	MT158755	Fernández-López & al. 2020
<i>X. raduloides</i>	KAS-JR26	MH880225	MH884910	Riebesehl & al. 2019
<i>X. reticulatus</i>	GC 1512-1	KX857808	KX857813	Chen & al. 2017
<i>X. rhizomorphus</i>	Dai 12354	KF917544	—	Zhao & al. 2014
<i>X. rimosissimus</i>	Ryberg 021031	DQ873627	—	Larsson & al. 2006
<i>X. serpentiformis</i>	TUB-FO 40688	MH880229	—	Riebesehl & al. 2019
<i>X. spathulatus</i>	MSK-F 12931	MH884914	MH880231	Riebesehl & al. 2019
<i>X. subclavatus</i>	TUB-FO 42167	MH880232	—	Riebesehl & al. 2019
<i>X. subflaviporus</i>	Wu 0809-76	KX857803	KX857815	Chen & al. 2018
<i>X. subtropicus</i>	Wu 9806-105	KX857807	KX857809	Chen & al. 2017
<i>X. verecundus</i>	KHL 12261	DQ873642	—	Larsson & al. 2006

and ITS4 (White & al. 1990), and the nLSU region was amplified with primer pairs LR0R and LR7 (<http://lutzonilab.org/nuclear-ribosomal-dna>). The ITS PCR protocol was: initial denaturation at 95 °C for 3 min; then 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min; and a final extension of 72 °C for 10 min. The nLSU PCR protocol was: initial denaturation at 94 °C for 1 min; then 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min; and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (TABLE 1).

Sequencher 4.6 (<https://www.genecodes.com>) was used to edit the DNA sequence. Sequences were aligned using the “G-INS-I” strategy in MAFFT 7 (<https://mafft.cbrc.jp/alignment/server/>) and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 28085). The outgroup *Hastodontia halonata* (J. Erikss. & Hjortstam) Hjortstam & Ryvar den

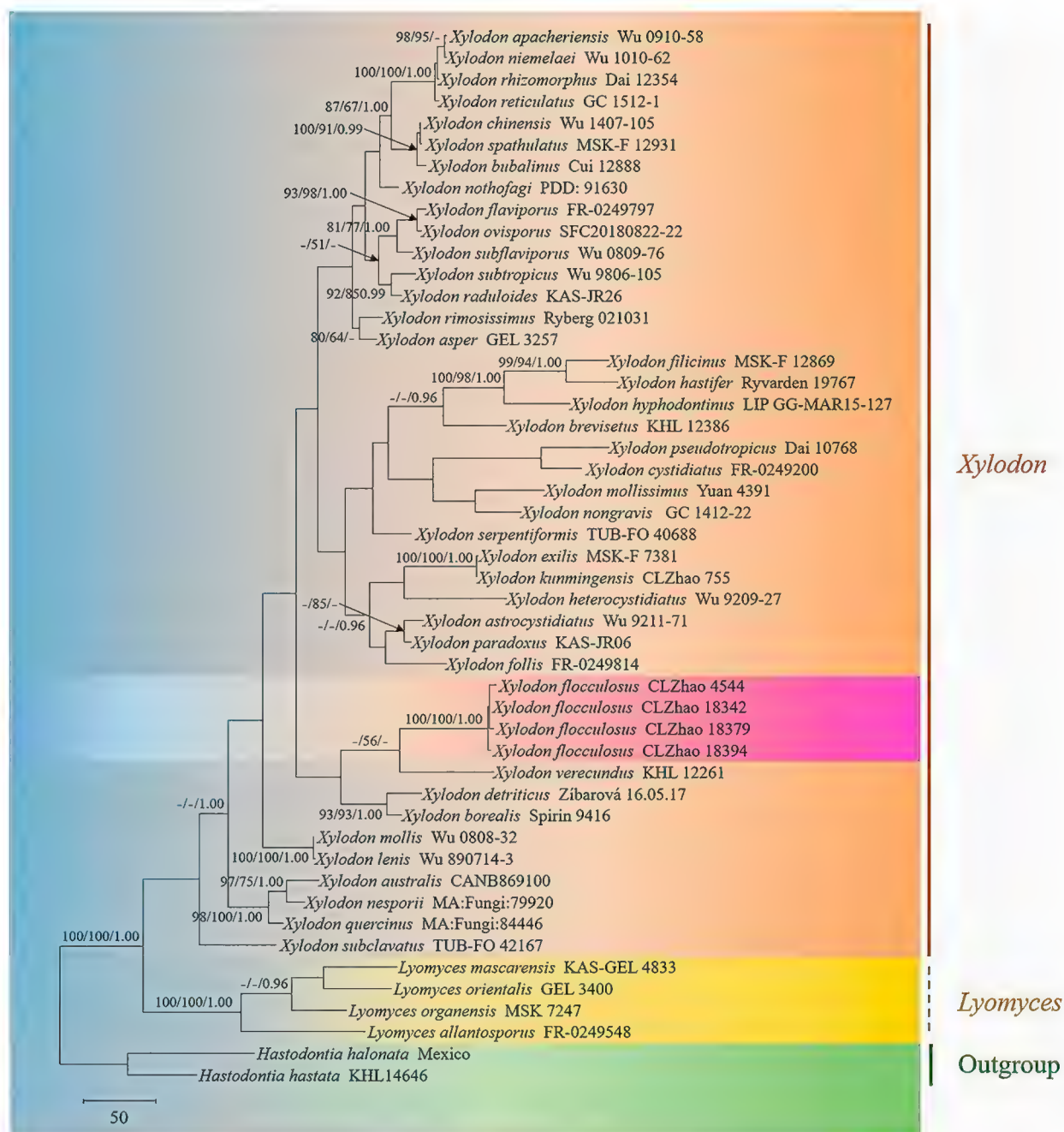


FIG. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Xylodon flocculosus* and related species in the residual polyporoid clade, based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.

and *H. hastata* (Litsch.) Hjortstam & Ryvarden was used to root the tree in the combined analyses following Shi & al. (2019) (FIG. 1).

Maximum parsimony (MP) analysis was applied to the combined dataset sequences. Approaches to phylogenetic analysis followed Zhao & Wu (2017), and the tree was generated in PAUP* 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap

(BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each MP tree generated. Sequences were also analyzed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org, Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicate.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian Inference (BI). BI was calculated with MrBayes 3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 1.4 million generations, with trees sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree was calculated for all remaining trees. Branches were considered as significantly supported if they received a maximum likelihood bootstrap value (BS) >70%, maximum parsimony bootstrap value (BT) >50%, or Bayesian posterior probabilities (BPP) >0.95.

Molecular phylogeny

The combined ITS+nLSU dataset included sequences from 49 fungal specimens representing 46 taxa. The dataset had an aligned length of 2617 characters, of which 960 characters were constant, 208 parsimony-uninformative and 428 parsimony-informative. MP analysis yielded 1 equally parsimonious tree (TL = 2617, CI = 0.380, HI = 0.620, RI = 0.481, RC = 0.183). The best-fit model for ITS+nLSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI analysis produced a similar topology with an average standard deviation of split frequencies = 0.009310.

The phylogenetic tree (FIG. 1) inferred from ITS+nLSU sequences includes 46 *Xylodon* species. *Xylodon flocculosus* formed a well-supported distinct lineage and was sister to *X. verecundus* (G. Cunn.) Yurchenko & Riebesehl.

Taxonomy

Xylodon flocculosus C.L. Zhao, sp. nov.

FIGS 2, 3

MB 840651

Differs from *Xylodon verecundus* by its grandinoid hymenial surface and strongly encrusted cystidia.

TYPE: China. Yunnan Province: Honghe, Pingbian County, Daweishan National Nature Reserve, on a fallen angiosperm branch, 3 Aug 2019, CLZhao 18342 (Holotype, SWFC 0018342; GenBank MW980776, MW980779).

ETYMOLOGY: *flocculosus* (Lat.) refers to the flocculent hymenophore of the type specimen.

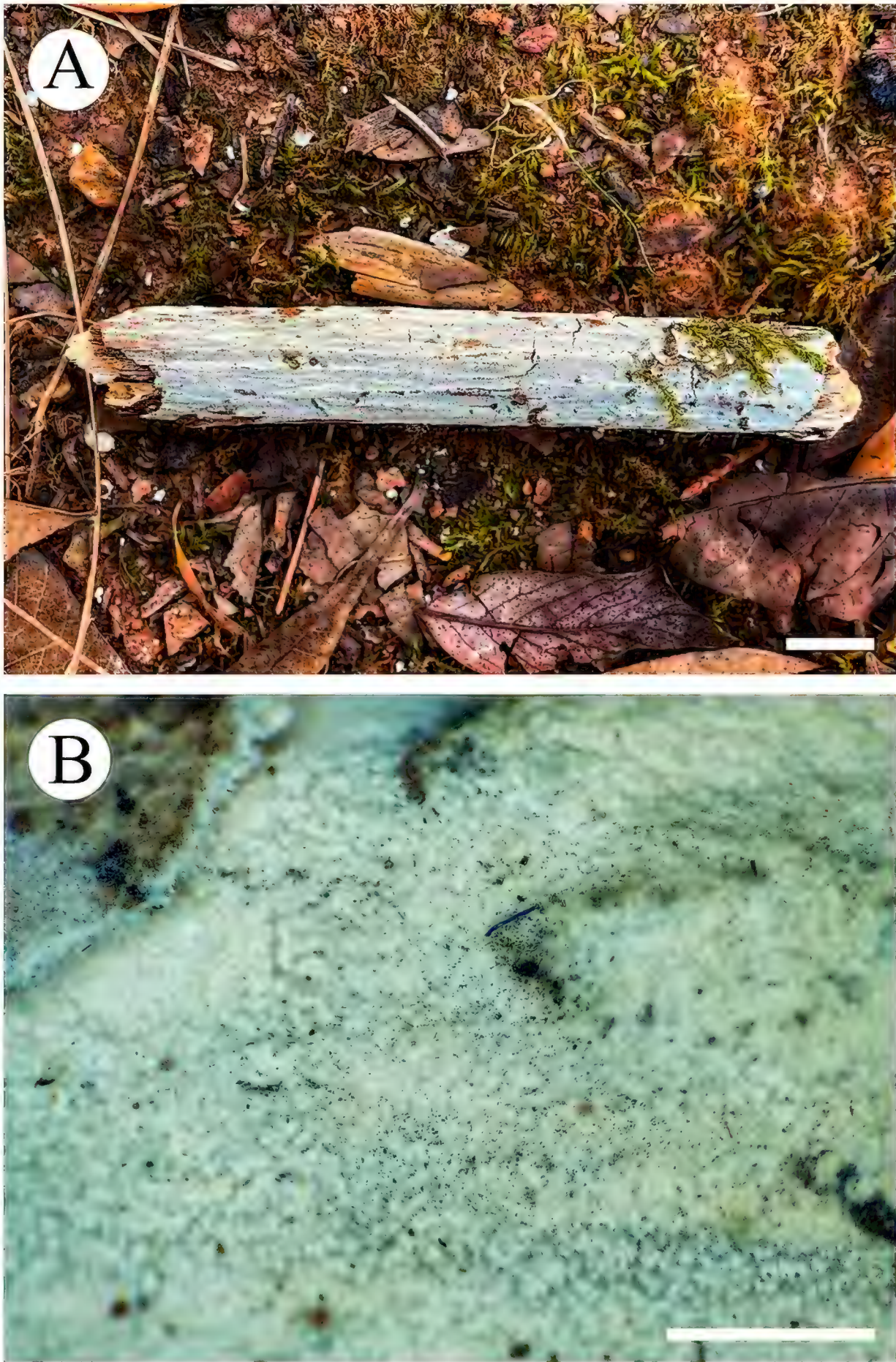


FIG. 2. *Xylodon flocculosus* (holotype, SWFC 0018342).
Basidiomata. Scale bars: A = 1 cm; B = 1 mm.

BASIDIOMATA annual, resupinate, soft, cottony, without odor or taste when fresh, becoming flocculent on drying, $\leq 10 \times 3$ cm (length $\times$ breadth), ≤ 200 μ m thick. Hymenial surface grandinoid, aculei 15–20 per mm, 50–100 μ m long, white to pale buff when fresh, turn to buff upon drying. Margin sterile, white to pale buff, ≤ 1 mm wide.

HYPHAL STRUCTURE monomitic; generative hyphae clamped, hyaline, more or less interwoven, thick-walled, branched, 2–3 μ m in diameter; IKI–, CB–, tissues unchanged in KOH.

HYMENIUM Cystidia numerous in the aculei, strongly encrusted at the obtuse apex, $22\text{--}55 \times 2.9\text{--}5.6$ μ m; cystidioles absent; basidia barrel-shaped, with four sterigmata, basally clamped, slightly constricted in the middle to somewhat sinuous, $11\text{--}20 \times 3.3\text{--}4.8$ μ m; basidioles dominant, in shape similar to basidia, but slightly smaller.

BASIDIOSPORES ellipsoid, hyaline, thick-walled, smooth, IKI–, CB–, $(4\text{--})4.2\text{--}5.7$ $(-6) \times 3.1\text{--}4.4(-4.6)$ μ m, $L = 4.92$ μ m, $W = 3.57$ μ m, $Q = 1.35\text{--}1.42$ ($n = 120/4$).

TYPE OF ROT: white rot.

ADDITIONAL SPECIMENS EXAMINED: CHINA. YUNNAN PROVINCE. Puer: JINGDONG COUNTY, Wuliangshan National Nature Reserve, on fallen angiosperm branch, 6 Oct 2017, CLZhao 4544 (SWFC 004544; GenBank MW980775). Honghe: PINGBIAN COUNTY, Daweishan National Nature Reserve, on fallen angiosperm branch, 3 Aug 2019, CLZhao 18379 (SWFC 018379; GenBank MW980777, MW980780) CLZhao 18394 (SWFC 018394; GenBank MW980778, MW980781).

Discussion

Earlier morphological and molecular studies (Yurchenko & Wu 2014, Riebesehl & al. 2019) strongly supported *Xylodon* as an independent genus in the *Xylodon-Schizopora-Palifer* clade. The newly described *X. flocculosus* is nested in *Xylodon* (FIG. 1) based on the combined ITS+nLSU sequence data (BS = 100%, BT = 100%, BPP = 1). The usefulness of the ITS region alone to delimit species in *Xylodon* is approaching its phylogenetic limits. Riebesehl & al. (2019) called for additional genetic markers in *Xylodon*. The present study, based on ITS and nLSU sequences, supports *X. flocculosus* within a distinct, well-supported monophyletic lineage. In ITS phylogenetic tree, *Xylodon flocculosus* was sister to *X. verecundus*. However, morphologically *X. verecundus* differs from *X. flocculosus* in its alutaceous hymenial surface, capitate cystidia, and narrower basidiospores (5×3 μ m; Hjortstam & Ryvarden 1997).

Morphologically, *Xylodon flocculosus* resembles *X. australis* (Berk.) Hjortstam & Ryvarden, *X. rimosissimus* (Peck) Hjortstam & Ryvarden,

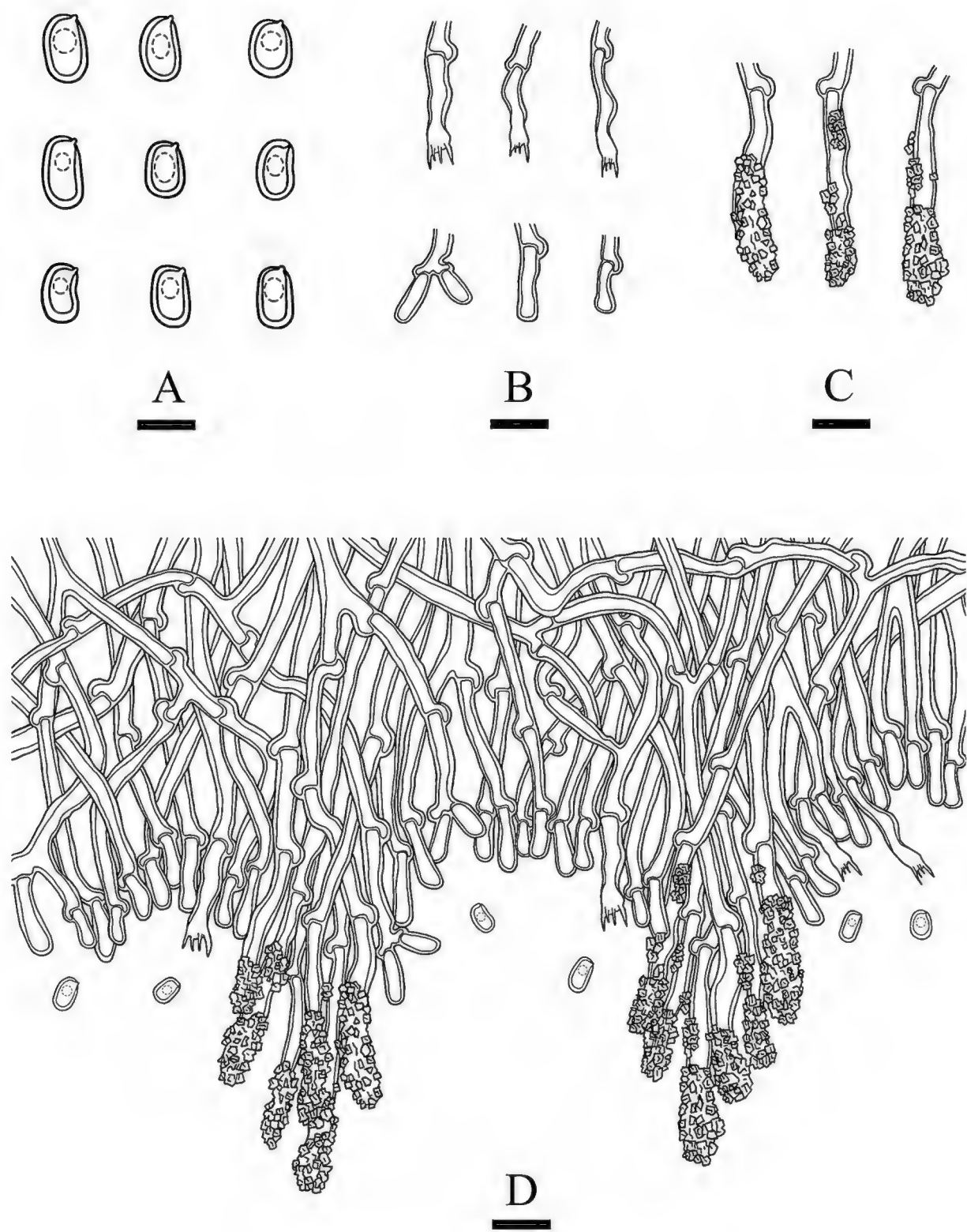


FIG. 3. *Xylodon flocculosus* (holotype, SWFC 0018342).
A. Basidiospores; B. Basidia and basidioles; C. Encrusted cystidia;
D. Section of hymenium. Scale bars: A = 5 µm; B–D = 10 µm.

and *X. tenellus* Hjortstam & Ryvar den in sharing a grandinoid hymenial surface. *Xylodon australis* differs in having hymenophore cracked into small polygons and larger basidiospores ($6\text{--}7.5 \times 4\text{--}4.5\text{ }\mu\text{m}$, Riebesehl & al. 2019);

X. rimosissimus is distinguished by its cream to beige, slightly orange hymenial surface and capitate cystidia (Langer 1994); and *X. tenellus* differs in its smaller globose basidiospores ($4\text{--}4.2 \times 4.2\text{--}4.5 \mu\text{m}$, Hjortstam & Ryvarden 2007).

Xylodon fimbriatus (Sheng H. Wu) Hjortstam & Ryvarden, nom. illeg. [$\equiv$ *Lyomyces fimbriatus* (Sheng H. Wu) Riebesehl & Yurchenko (Yurchenko & al. 2020)], *X. papillosus* (Fr.) Riebesehl & al., and *X. subflaviporus* C.C. Chen & Sheng H. Wu also resemble *X. flocculosus* in having strongly encrusted cystidia. However, *X. fimbriatus* is distinguished by its limy-white hymenophore and capitate cystidia (Langer 1994), *X. papillosus* by its smooth or finely odontoid hymenophore (Rattan 1977), and *X. subflaviporus* by its poroid hymenophore with cream to straw-colored hymenial surface and apically encrusted cystidia (Chen & al. 2018).

Xylodon archeri (Berk.) Kuntze, *X. lenis* Hjortstam & Ryvarden, and *X. tuberculatus* (Kotir. & Saaren.) Hjortstam & Ryvarden are also reported with ellipsoid basidiospores. *Xylodon archeri* differs in its coralloid basidiomata with cinnamon-buff or buckthorn brown hymenial surface and presence of the capitate cystidia (Nakasone 2012), *X. lenis* in its pinkish-tinted ochraceous hymenophore and moniliform cystidia (Langer 1994), and *X. tuberculatus* in its smooth to papillose or tuberculate hymenophore and presence of gloecystidia (Kotiranta & Saarenoksa 2000).

Acknowledgments

Special thanks are due to Drs. Avneet Pal Singh (Department of Botany, Punjabi University, Patiala, India) and Mei-Ling Han (College of Life Science, Langfang Normal University, Langfang, P.R. China) who reviewed the manuscript. The research was supported by the National Natural Science Foundation of China (Project No. 32170004), Yunnan Fundamental Research Project (Grant No. 202001AS070043), Key Laboratory of Forest Resources Conservation and Utilization in the Southwest Mountains of China Ministry of Education, Southwest Forestry University (KLESWFU-202003), and the National College Students Innovation and Entrepreneurship Training Program (No. 202110677002).

Literature cited

- Bernicchia A, Gorjón SP. 2010. Fungi Europaei 12: *Corticiaceae* I. Edizioni Candusso, Lomazzo. 1007 p.
- Boidin J, Gilles G. 2003. *Homobasidiomycètes Aphyllophorales* non porés à basides dominantes à 2 (3) stérigmates. Bulletin Trimestriel de la Société Mycologique de France 119: 1–17.
- Burdsall HH, Nakasone KK, Freeman GW. 1981. New species of *Gloeocystidiellum* (*Corticiaceae*) from the southeastern United States. Systematic Botany 6: 422–434. <https://doi.org/10.2307/2418453>

- Chen JJ, Zhou LW, Ji XH, Zhao CL. 2016. *Hyphodontia dimitica* and *H. subefibulata* spp. nov. (*Schizoporaceae*, *Hymenochaetales*) from southern China based on morphological and molecular characters. *Phytotaxa* 269: 1–13. <https://doi.org/10.11646/phytotaxa.269.1.1>
- Chen CC, Wu SH, Chen CY. 2017. Three new species of *Hyphodontia* s.l. (*Basidiomycota*) with poroid or raduloid hymenophore. *Mycological Progress* 16: 553–564. <https://doi.org/10.1007/s11557-017-1286-0>
- Chen CC, Wu SH, Chen CY. 2018. *Xylodon subflaviporus* sp. nov. (*Hymenochaetales*, *Basidiomycota*) from East Asia. *Mycoscience* 59: 343–352. <https://doi.org/10.1016/j.myc.2017.12.004>
- Dai YC. 2011. A revised checklist of corticioid and hydroid fungi in China for 2010. *Mycoscience* 52: 69–79. <https://doi.org/10.1007/S10267-010-0068-1>
- Dai YC. 2012. Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49–80. <http://doi.org/10.1007/s10267-011-0134-3>
- Eriksson J, Ryvarden L. 1976. The *Corticiaceae* of North Europe volume 4, *Hyphodermella–Mycoacia*. Fungiflora, Oslo
- Felsenstein J. 1985. Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39: 783–791. <https://doi.org/10.2307/2408678>
- Fernández-López J, Telleria MT, Dueñas M, Laguna-Castro M, Schlep K, Martín MP. 2020. Linking morphological and molecular sources to disentangle the case of *Xylodon australis*. *Scientific Reports* 10(22004): [14 p.]. <https://doi.org/10.1038/s41598-020-78399-8>
- Fukami T, Dickie IA, Wilkie JP, Paulus BC, Park D, Roberts A, Buchanan PK, Allen RB. 2010. Assembly history dictates ecosystem functioning: evidence from wood decomposer communities. *Ecology Letters* 13: 675–648. <https://doi.org/10.1111/j.1461-0248.2010.01465.x>
- Gray SF. 1821. A natural arrangement of British plants. London: Nabu Press.
- Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Hjortstam K, Ryvarden L. 1997. Corticioid species (*Basidiomycotina*, *Aphyllophorales*) from Colombia collected by Leif Ryvarden. *Mycotaxon* 64: 229–241.
- Hjortstam K, Ryvarden L. 2007. Studies in corticioid fungi from Venezuela III (*Basidiomycotina*, *Aphyllophorales*). *Synopsis Fungorum* 23: 56–107.
- Hjortstam K, Ryvarden L, Iturriaga T. 2005. Studies in corticioid fungi from Venezuela II (*Basidiomycotina*, *Aphyllophorales*). *Synopsis Fungorum* 20: 42–78.
- Jo JW, Kwag YN, Cho SE, Han SK, Han JG, Oh S, Kim CS. 2019. *Xylodon flaviporus*, a newly recorded macrofungi in Dokdo, South Korea. *Korean Journal of Mycology* 47(3): 241–247. <https://doi.org/10.4489/KJM.20190028>
- Kan YH, Gafforov Y, Li T, Zhou LW. 2017a. *Hyphodontia zhixiangii* sp. nov. (*Schizoporaceae*, *Basidiomycota*) from Uzbekistan. *Phytotaxa* 299: 273–279. <https://doi.org/10.11646/phytotaxa.299.2.12>
- Kan YH, Qin WM, Zhou LW. 2017b. *Hyphodontia mollissima* sp. nov. (*Schizoporaceae*, *Hymenochaetales*) from Hainan, southern China. *Mycoscience*. <https://doi.org/10.1016/j.myc.2017.04.003>
- Kotiranta H, Saarenoksa R. 2000. Three new species of *Hyphodontia* (*Corticiaceae*). *Annales Botanici Fennici* 37: 255–278.
- Langer E. 1994. Die Gattung *Hyphodontia* John Eriksson. *Bibliotheca Mycologica* 154. 298 p.
- Larsson KH, Parmasto E, Fischer M, Langer E, Nakasone KK, Redhead SA. 2006. *Hymenochaetales*: a molecular phylogeny for the hymenochaetoid clade. *Mycologia* 98: 926–936. <https://doi.org/10.3852/mycologia.98.6.926>

- Lee IS, Langer E. 2012. New records of *Hyphodontia* species from Taiwan. *Nova Hedwigia* 94: 239–244. <https://doi.org/10.1127/0029-5035/2012/0094-0239>
- Lupala AS, Oh S-Y, Park MS, Kim T, Yoo J-S, Seelan JSS, Lim YW. 2019. Co-occurrence patterns of wood-decaying fungi and ants in dead pines of South Korea. *Journal of Asia-Pacific Entomology* 22: 1154–1160. <https://doi.org/10.1016/j.aspen.2019.10.009>
- Ma X, Zhao CL. 2021. *Xylodon bambusinus* and *X. xinpingensis* spp. nov. (*Hymenochaetales*) from southern China. *Phytotaxa* 511: 231–247. <https://doi.org/10.11646/phytotaxa.511.3.3>
- Miller MA, Holder MT, Vos R, Midford PE, Liebowitz T, Chan L, Hoover P, Warnow T. 2009. The CIPRES Portals. CIPRES. http://www.phylo.org/sub_sections/portal. 2009-08-04. (Archived by WebCite® at <https://www.webcitation.org/5imQlJeQa>).
- Nakasone KK. 2012. Type studies of corticioid *Hymenomycetes* (*Basidiomycota*) with aculei—part II. *Czech Mycology* 64: 23–42. <https://doi.org/10.33585/cmy.64104>
- Nordén B, Appelquist T, Lindahl B, Henningsson M. 1999. Cubic rot fungi – corticioid fungi in highly brown rotted spruce stumps. *Mycologia Helvetica* 10: 13–24.
- Nylander JAA. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala.
- Petersen JH. 1996. Farvekort. The Danish Mycological Society's colour-chart. Foreningen til Svampekundskabens Fremme, Greve.
- Rattan SS. 1977. The resupinate *Aphyllorphorales* of the northwestern Himalayas. *Bibliotheca Mycologica* 60. 427 p.
- Riebesehl J, Langer E. 2017. *Hyphodontia* s.l. (*Hymenochaetales*, *Basidiomycota*): 35 new combinations and new keys to all 120 current species. *Mycological Progress* 16: 637–666. <https://doi.org/10.1007/s11557-017-1299-8>
- Riebesehl J, Yurchenko E, Nakasone KK, Langer E. 2019. Phylogenetic and morphological studies in *Xylodon* (*Hymenochaetales*, *Basidiomycota*) with the addition of four new species. *MycKeys* 47: 97–137. <https://doi.org/10.3897/mycokeys.47.31130>
- Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572–1574. <https://doi.org/10.1093/bioinformatics/btg180>
- Shi ZW, Wang XW, Zhou LW, Zhao CL. 2019. *Xylodon kunmingensis* sp. nov. (*Hymenochaetales*, *Basidiomycota*) from southern China. *Mycoscience* 60(3): 184–188. <https://doi.org/10.1016/j.myc.2019.02.002>
- Swofford DL. 2002. PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Massachusetts: Sinauer Associates.
- Viner I, Spirin V, Zibarová L, Larsson K-H. 2018. Additions to the taxonomy of *Lagarobasidium* and *Xylodon* (*Hymenochaetales*, *Basidiomycota*). *MycKeys* 41: 65–90. <https://doi.org/10.3897/mycokeys.41.28987>
- Wang M, Chen YY. 2017. Phylogeny and taxonomy of the genus *Hyphodontia* (*Hymenochaetales*, *Basidiomycota*) in China. *Phytotaxa* 309: 45–54. <https://doi.org/10.11646/phytotaxa.309.1.4>
- Wang XW, May TW, Liu SL, Zhou LW. 2021. Towards a natural classification of *Hyphodontia* sensu lato and the trait evolution of basidiocarps within *Hymenochaetales* (*Basidiomycota*). *Journal of Fungi* 7(478): [76 p.]. <https://doi.org/10.3390/jof7060478>
- White TJ, Bruns TD, Lee SB, Taylor JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: MA Innis & al. (eds). PCR protocols: a guide to methods and applications. Academic Press, New York. <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>
- Wu SH. 1990. The *Corticiaceae* (*Basidiomycetes*) subfamilies *Phlebioideae*, *Phanerochaetoideae* and *Hyphodermoideae* in Taiwan. *Annales Botanici Fennici* 142. 123 p.

- Wu SH. 2000. Studies on *Schizopora flavipora* s.l., with special emphasis on specimens from Taiwan. *Mycotaxon* 76: 51–66.
- Wu SH. 2001. Three new species of *Hyphodontia* with poroid hymenial surface. *Mycologia* 93: 1019–1025. <https://doi.org/10.2307/3761766>
- Wu SH. 2006. *Hyphodontia tubuliformis*, a new species from Taiwan. *Mycotaxon* 95: 185–188.
- Xiong HX, Dai YC, Wu SH. 2009. Three new species of *Hyphodontia* from Taiwan. *Mycological Progress* 8: 165–169. <https://doi.org/10.1007/s11557-009-0587-3>
- Xiong HX, Dai YC, Wu SH. 2010. Two new species of *Hyphodontia* from China. *Mycologia* 102: 918–922. <https://doi.org/10.3852/09-139>
- Yurchenko E, Xiong HX, Wu SH. 2013. Four new species of *Hyphodontia* (*Xylodon* s.s. Hjortstam & Ryvar den, *Basidiomycota*) from Taiwan. *Nova Hedwigia* 96: 545–558. <https://doi.org/10.1127/0029-5035/2013/0092>
- Yurchenko E, Wu SH. 2014. Three new species of *Hyphodontia* with peg-like hyphal aggregations. *Mycological Progress* 13: 533–545. <https://doi.org/10.1007/s11557-013-0935-1>
- Yurchenko E, Riebesehl J, Langer E. 2017. Clarification of *Lyomyces sambuci* complex with the descriptions of four new species. *Mycological Progress* 16: 865–876. <https://doi.org/10.1007/s11557-017-1321-1>
- Yurchenko E, Riebesehl J, Langer E. 2020. *Fasciodontia* gen. nov. (*Hymenochaetales*, *Basidiomycota*) and the taxonomic status of *Deviodontia*. *Mycological Progress* 19: 171–184. <https://doi.org/10.1007/s11557-019-01554-7>
- Zhao CL, Wu ZQ. 2017. *Ceriporiopsis kunmingensis* sp. nov. (*Polyporales*, *Basidiomycota*) evidenced by morphological characters and phylogenetic analysis. *Mycological Progress* 16: 93–100. <https://doi.org/10.1007/s11557-016-1259-8>
- Zhao CL, Cui BK, Dai YC. 2014. Morphological and molecular identification of two new species of *Hyphodontia* (*Schizoporaceae*, *Hymenochaetales*) from southern China. *Cryptogamie Mycologie* 35: 87–97. <https://doi.org/10.7872/crym.v35.iss1.2014.87>